SUPPLEMENTARY FIGURES 1 & 2

grim promotes programmed cell death of *Drosophila* microchaete glial cells



Supplementary Figure 1:

The glutamine-rich domain is amino-terminal to a highly conserved region.

Alignment of Grim from all sequenced Drosophila species was performed using ClustalW. Boxed regions are regions of high identity. Within these boxed regions, identical amino acids are shaded dark gray and conservative substitutions are shaded light gray. Residues with no shading are non-conservative substitutions although occasionally subfamilies can be seen within these regions. The extent of the protein domains (IBM, GH3 and glutamine-rich) are shown. Note that the glutamine-rich domain is shaded light gray and no attempt was made to highlight identities within this region as it is of variable length.

The extent of the deletion in the Grim^{$\Delta52-57$} mutation is marked by carets above the *D.* melanogaster sequence. Removal of the 6 amino acids in the mutant, 4 of them charged residues, could have a specific deleterious effect on Grim proapoptotic function, or could impact Grim by reducing the size of the glutamine-rich domain.



Supplementary Figure 2:

Loss of *buffy* does not lead to increased cell division when *grim* is expressed.

Mitotic cells posterior to the morphogenetic furrow were identified using an antiphosphohistone H3 antibody on eye discs dissected from wandering third instar larvae grown at 29°C. A previous study also demonstrated no effect of loss of *buffy* on cell division (Sevrioukov *et al.* Genesis 2005). The number of mitotic cells per eye disc was counted. Shown is the mean and SEM (N=11 for *GMR-grim* and N=10 for *buffy*^{H37}; *GMRgrim*). The difference between the genotypes is not significant based on an unpaired twotailed Student's *t* test.